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Jytte Hansen

Jytte Hansen
Kontorfuldmægtig

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Titel: Metode til detektion af patogene E.coli ved anvendelse af TaqMan™ PCR

Ansøger: Bavarian Nordic Research Institute
Smedeland 26B
2600 Glostrup

Opfindere: Klaus Pfeffer
Klaus Heeg
Hermann Wagner

TaqMan™-PCR for the detection of pathogenic E.coli strains

The present invention relates to a rapid, high performance assay for the detection of pathogenic E.coli which is based on TaqMan™ PCR technique, and to specific optimised oligonucleotide primers and labelled oligonucleotide probes useful in the assay.

Background of the Invention

Enterohemorrhagic, shiga-like toxin (slt) producing *Escherichia coli* (EHEC) have recently been recognized as an important human and animal pathogen (1-7). EHEC has been responsible for several food-borne outbreaks (8). The most notable were a multistate outbreak associated with a fast food chain in the western states of the USA with more than 600 individuals affected and 3 deaths in Washington (9), and an epedemic occurence in Japan with more than 6000 patients and approx. 8 fatal cases (10). Infection with EHEC causes diarrhea, hemorrhagic colitis, thrombotic thrombocytopenic purpura, and hemolytic uremic syndrome (HUS) that is characterised by acute renal failure, thrombocytopenia, and microangiopathic hemolytic anemia. HUS ultimately can result in a fatal outcome in affected children and immunocompromised individuals (3,11-17). Recently, in the South-Eastern parts of Germany (Bavaria) an increase of EHEC cases was reported during October 1995 and July 1996 with at least 45 severe infections leading to HUS accompanied by 7 deaths (18). Estimating that approx. 1 out of 15 EHEC infections results in HUS approx. 600 - 700 affected individuals might be assumed.
In most outbreaks reported, consumption of contaminated ground beef has been the source of infection (5,8,19-22), whereas in Japan raddish sprouts are suspected (10). EHEC has been isolated from cow milk (6,19,23), water (19), chicken, pork, and apple cider (19,24,25), but also human horizontal smear infections have been reported (15). Cattle appear likely to be the reservoir (22,26). Cross contamination, improper handling, and inadequate cooking all contribute to food-borne infections caused by EHEC. EHEC produce Shiga-like toxins (slt), also known as verotoxins or cytotoxins (12,27). A large proportion of EHEC have been found to belong to the serogroup O157:H7, but notably, also a variety of EHEC belonging to other serogroups (O22, O26, O55, O111, O114, O145) have been reported especially in Europe (12,15,28-32).

Besides EHEC, certain other strains of *E.coli* can cause enteritis or gastroenteritis and are grouped in enterotoxigenic strains (ETEC) (33-36), enteropathogenic strains (EPEC) (37), enteroinvasive strains (EIEC) (38,39), and enteroaggregative strains (EaggEC) (40,41). These strains are important pathogens and also pose severe public health problems. The diagnosis of these pathogens is vastly neglegted due to the lack of specific and sensitive routine test methods. ETEC synthesize heat labile and/or heat stable enterotoxins that can cause a secretory diarrhea ("traveller's diarrhea") resembling that of *Vibrio cholerae* (36,42,43). Surface attachment of the ETEC organisms to the intestinal epithelial cell is a prerequisite to toxin production. Toxin production is plasmid mediated and most commonly involves *E.coli* serogroups O6, O15, O124, O136, O143, O145, and O147 (32).

EPEC cause diarrheal symptoms primarily in infants (32). Although the pathogenesis is unclear, the epithelial degradation of the gut, and the inflammatory response that are observed in tissue sections may be a consequence due to the adhesive properties of the bacterium. Specific attachment factors of EPEC are plasmid encoded (EAF=EPEC adherence factor) (37,44). EHEC often contain an adherence factor closely related to EAF that is known as *eae* (EHEC attaching and effacing gene) (45,46). EPEC most often belong to serogroups O6, O8, O25, O111, O119, and O142 (32).

EIEC strains are capable of penetrating and invading the intestinal epithelial cells and produce an inflammatory diarrhea similar to that caused by *Shigella* bacteria (38,47,48). Fecal smears contain blood, mucus and segmented neutrophils. EIEC contain virulence plasmids coding for additional pathogenic factors (48). Serogroups O28, O112, O115, O124, O136, O143, O145, and O147 are most commonly found on EIEC (32).

EaggEC are associated with persistent diarrhea in children and with traveller's diarrhea. EaggEC are characterized by their adherence capacity that leads to aggregation of Hep-2 cells. This effect is associated with the presence of a virulence plasmid (pCVD432). EaggEC are supected to also produce a heat stable enterotoxin (EAST1) (49-53). They can belong to serogroups O44 and O126 (32).

Conventional detection methods for EHEC encompass enrichment and isolation with selective and/or indicator media such as E.coli broth, lauryl sulfate tryptose 4-methylumbelliferyl-b-acid broth, eosin methylene blue agar, McConkey sorbitol agar, and enterohemolysin agar (28,32,54-59). All of these assays, unfortunately, are indirect and lack the ability to identify EHEC or the other pathogenic *E.coli* strains

specifically. Several methods for biochemical identification and immunological detection of EHEC have been put forward (54,60-63), however, it is well recognized that pathogenic *E.coli* strains neither posess nor lack unique fermentation pathways (58,64). Serotyping is not conclusive since no absolute correlation between serotype and pathogenic *E.coli* group can be established (12,27,32,58,65).

DNA hybridization techniques have been established for experimental research but are not applicable for large scale routine diagnostic procedures (66,67). DNA amplification based assays, using PCR have been reported (68-72). Limitations to these methods include cumbersome post-PCR detection methods (agarose gel electrophoresis, Biotin/Avidin based ELISA detection systems).

To overcome these problems, a PCR assay which allows the specific determination of virulence factors characteristic for EHEC, ETEC, EPEC, EIEC, and EaggEC that is based on a fluorigenic detection method of PCR amplification has been developed.

This assay exploits the 5´ → 3´exonuclease activity of Taq-DNA polymerase (73) to cleave an internal oligonucleotide probe that is covalently conjugated with a fluorescent reporter dye (e.g. 6-carboxy-fluorescein [FAM]; λ_{em} = 518nm) and a fluorescent quencher dye (6-carboxytetram-ethyl-rhodamine [TAMRA]; λ_{em} = 582nm) at the 5´ and 3´end, respectively (74,75). Fluorescence from FAM is efficiently quenched by TAMRA on the same, intact probe molecule (76). In the case that cognate PCR amplification occurs, Taq polymerase extends from the specific PCR primer and cleaves the internal, fluorigenic oligonucleotide probe annealed to the template strand. Thus, the reporter dye and the quencher dye get spatially separated. As a consequence of oligonucleotide hydrolysis and physical separation of the reporter and the quencher dyes, a measurable increase in fluoresecence intensity at 518 nm can be observed. PCR cycling leads to exponential amplification of the PCR product and consequently of fluorescence intensity.

TaqMan™-PCR is performed in optical tubes that allow measurements of fluorescence signals without opening the PCR tubes. This dramatically minimizes post-PCR processing time and almost completely eliminates cross-PCR contamination problems. Employing this approach, simultaneous testing of biological materials for the presence of virulence genes of *E.coli* strains and other

enterobacteria, harboring virulence genes can be semiautomated and performed within 18 h.

According to the present invention TaqMan™-PCR for the detection of pathogenic *E.coli* is provided, enabling for the first time the specific, rapid and high throughput routine detection of EHEC, ETEC, EPEC, EIEC, and EaggEC and related enterobacteria that harbor these virulence genes in routine bacteriological laboratories.

Object of the Invention

It is an object of the present invention to provide a rapid, high performance assay for the detection and identification of pathogenic E.coli in biological samples.

It is a further object of the present invention to provide specific, optimised primers and labelled oligonucleotide probes useful for the amplification of sequences encoding virulence factors/toxins characteristic for pathogenic E.coli

Summary of the Invention

The invention then, inter alia, comprises the following alone or in combination:

A method for the detection of pathogenic E. coli in a sample comprising PCR amplification of DNA isolated from said sample using a set of oligonucleotide primers specific for virulence factors/toxins of pathogenic E.coli selected from

primers that hybridise to the gene encoding labile heat toxin, or stabile heat toxin for the amplification of a DNA sequence characteristic for enterotoxigenic E.coli;

primers that hybridise to the pCVD432 plasmid for the amplification of a DNA sequence characteristic for enteroaggregative E.coli;

primers that hybridise to the inv-plasmid for the amplification of a DNA sequence contained in enteroinvasive E.coli;

primers that hybridise to the EAF plasmid, or the eae gene for the amplification of a DNA sequence characteristic for enteropathogenic E.coli; and/or

primers that hybridise to the genes encoding shiga-like toxin sltI or sltII for the amplification of a DNA sequence characteristic for enterohemorrhagic E.coli, followed by detection and identification of the amplified product using conventional methods;

a method as above wherein

the set of primers that hybridise to the gene encoding labile heat toxin is

LT-1: $^{5'}$ GCG TTA CTA TCC TCT CTA TGT G $^{3'}$ and
LT-2: $^{5'}$ AGT TTT CCA TAC TGA TTG CCG C $^{3'}$;

the set of primers that hybridise to the gene encoding stabile heat toxin is

ST-1: $^{5'}$ TCC CTC AGG ATG CTA AAC CAG $^{3'}$ and
ST-2a: $^{5'}$ TCG ATT TAT TCA ACA AAG CAA C $^{3'}$;

the set of primers which hybridise to the pCVD432 plasmid is

EA-1: $^{5'}$ CTG GCG AAA GAC TGT ATC ATT G $^{3'}$ and
EA-2: $^{5'}$ TAA TGT ATA GAA ATC CGC TGT T $^{3'}$;

the set of primers which hybridise to the inv-plasmid is

EI-1: $^{5'}$ TTT CTG GAT GGT ATG GTG AGG $^{3'}$ and
EI-2: $^{5'}$ CTT GAA CAT AAG GAA ATA AAC $^{3'}$;

the set of primers which hybridise to the EAF plasmid is

EP-1: $^{5'}$ CAG GGT AAA AGA AAG ATG ATA AG $^{3'}$ and
EP-2: $^{5'}$ AAT ATG GGG ACC ATG TAT TAT C $^{3'}$;

the set of primers which hybridise to the eae gene is

EPeh-1: $^{5'}$ CCC GGA CCC GGC ACA AGC ATA AG $^{3'}$ and

EPeh-2: $^{5'}$ AGT CTC GCC AGT ATT CGC CAC C $^{3'}$;

the primers which hybridises to the gene encoding shiga-like toxin SltI is

SltI-1: $^{5'}$ ATG AAA AAA ACA TTA TTA ATA GC $^{3'}$ and
SltI-2: $^{5'}$ TCA CYG AGC TAT TCT GAG TCA AGC $^{3'}$; and

the primers which hybridises to the gene encoding shiga-like toxin SltII is

SltII-1: $^{5'}$ ATG AAG AAG ATR WTT RTD GCR GYT TTA TTY G $^{3'}$ and
SltII-2: $^{5'}$ TCA GTC ATW ATT AAA CTK CAC YTS RGC AAA KCC $^{3'}$

wherein W is A/T, R is A/G, D is A/G/T, Y is C/T and K is G/T;

a method as above wherein a polymerase having additional 5'-3' exonuclease activity is used for the amplification of DNA, and an oligonucleotide probe labelled at the most 5' base with a fluorescent dye and at the most 3' base with a fluorescent quencher dye which hybridises within the target DNA is included in the amplification process; said labelled oligonucleotide probe being susceptible to 5'-3' exonuclease degradation by said polymerase to produce fragments that can be detected by fluorogenic detection methods;

a method as above wherein the labelled oligonucleotide probe for the detection of labile heat toxin is

$^{5'}$ AGC TCC CCA GTC TAT TAC AGA ACT ATG $^{3'}$;

the labelled oligonucleotide probe for the detection of stabile heat toxin is

$^{5'}$ ACA TAC GTT ACA GAC ATA ATC AGA ATC AG $^{3'}$;

the labelled oligonucleotide probe for the detection of pCVD432 plasmid is

$^{5'}$ CTC TTT TAA CTT ATG ATA TGT AAT GTC TGG $^{3'}$;

the labelled oligonucleotide probe for the detection of the inv-plasmid is;

$^{5'}$ CAA AAA CAG AAG AAC CTA TGT CTA CCT $^{3'}$

the labelled oligonucleotide probe for the detection of the EAF-plasmid is;

$^{5'}$ CTT GGA GTG ATC GAA CGG GAT CCA AAT $^{3'}$;

the labelled oligonucleotide probe for the detection of the eae gene is

$^{5'}$ TAA ACG GGT ATT ATC AAC AGA AAA ATC C $^{3'}$;

the labelled oligonucleotide probe for the detection of shiga-like toxin SItI gene is

$^{5'}$ TCG CTG AAT CCC CCT CCA TTA TGA CAG GCA $^{3'}$; and

the labelled oligonucleotide probe for the detection of shiga-like toxin SItII gene is

$^{5'}$ CAG GTA CTG GAT TTG ATT GTG ACA GTC ATT $^{3'}$;

a method as above wherein the fluoroscent reporter dye is 6-carboxy-fluoroscein, tetrachloro-6-carboxy-fluoroscein, or hexachloro-6-carboxy-fluoroscein, and the fluorescent quencher dye is 6-carboxytetramethyl-rhodamine;

a method as above wherein the PCR amplification process consists of 35 PCR cycles at a $MgCl_2$ concentration of 5.2 mmol, an annealing temperature of 55 °C and an extension temperature of 65 °C;

a method as above wherein the concentration of primers are 40 pmol and the concentration of labelled probe is 10 to 20 pmol;

a set of primers useful for PCR amplification of DNA specific for virulence factors/toxins of pathogenic E.coli selected from:

a set of primers that hybridise to the gene encoding labile heat toxin, or stabile heat toxin of enterotoxigenic E.coli;

a set of primers that hybridise to the pCVD432 plasmid of enteroaggregative E.coli;

a set of primers that hybridise to the inv-plasmid of enteroinvasive E.coli;

a set of primers that hybridise to the EAF plasmid, or the eae gene of enteropathogenic E.coli; and

a set of primers that hybridise to the gene encoding shiga-like toxin sltI or sltII of enterohemorrhagic E.coli;

a set of primers as above wherein

the set of primers which hybridise to the gene encoding labile heat toxin is

LT-1: $^{5'}$ GCG TTA CTA TCC TCT CTA TGT G ^{3} and
LT-2: $^{5'}$ AGT TTT CCA TAC TGA TTG CCG C $^{3'}$;

the set of primers which hybridise to the gene encoding stabile heat toxin is

ST-1: $^{5'}$ TCC CTC AGG ATG CTA AAC CAG $^{3'}$ and
ST-2a: $^{5'}$ TCG ATT TAT TCA ACA AAG CAA C $^{3'}$;

the set of primers which hybridise to the pCVD432 plasmid is

EA-1: $^{5'}$ CTG GCG AAA GAC TGT ATC ATT G $^{3'}$ and
EA-2: $^{5'}$ TAA TGT ATA GAA ATC CGC TGT T $^{3'}$;

the set of primers which hybridise to the inv-plasmid is

EI-1: $^{5'}$ TTT CTG GAT GGT ATG GTG AGG $^{3'}$ and
EI-2: $^{5'}$ CTT GAA CAT AAG GAA ATA AAC $^{3'}$;

the set of primers which hybridise to the EAF plasmid is

EP-1: $^{5'}$ CAG GGT AAA AGA AAG ATG ATA AG $^{3'}$ and
EP-2: $^{5'}$ AAT ATG GGG ACC ATG TAT TAT C $^{3'}$;

the set of primers which hybridise to the eae gene is

EPeh-1: $^{5'}$ CCC GGA CCC GGC ACA AGC ATA AG $^{3'}$ and
EPeh-2: $^{5'}$ AGT CTC GCC AGT ATT CGC CAC C $^{3'}$;

the set of primers which hybridise to the shiga-like toxin sltI gene is

SltI-1: $^{5'}$ ATG AAA AAA ACA TTA TTA ATA GC $^{3'}$ and
SltI-2: $^{5'}$ TCA CYG AGC TAT TCT GAG TCA AGC $^{3'}$;

and

the set of primers which hybridise to the shiga-like toxin sltII is

SltII-1: $^{5'}$ ATG AAG AAG ATR WTT RTD GCR GYT TTA TTY G $^{3'}$ and
SltII-2: $^{5'}$ TCA GTC ATW ATT AAA CTK CAC YTS RGC AAA KCC $^{3'}$

wherein W is A/T, R is A/G, D is A/G/T, Y is C/T and K is G/T.

a set of primers as above which in addition to the primers for amplification of target DNA comprise a labelled oligonucleotide probe which is
labelled with a fluoroscent reporter dye, such as 6-carboxy-fluoroscein, tetrachloro-6-carboxy-fluoroscein, hexachloro-6-carboxy-fluoroscein, at the most 5' base and a fluoroscent quencher dye, such as 6-carboxytetramethyl-rhodamine, at the most 3' base, and have a nucleotide sequence selected from

$^{5'}$ AGC TCC CCA GTC TAT TAC AGA ACT ATG $^{3'}$
which hybridises to the gene encoding labile heat toxin;

$^{5'}$ ACA TAC GTT ACA GAC ATA ATC AGA ATC AG $^{3'}$
which hybridises to the gene encoding stabile heat toxin;

$^{5'}$ CTC TTT TAA CTT ATG ATA TGT AAT GTC TGG $^{3'}$
which hybridises to the pCVD432 plasmid;

$^{5'}$ CAA AAA CAG AAG AAC CTA TGT CTA CCT $^{3'}$
which hybridises to the inv-plasmid;

$^{5'}$ CTT GGA GTG ATC GAA CGG GAT CCA AAT $^{3'}$
which hybridises to the EAF plasmid;

$^{5'}$ TAA ACG GGT ATT ATC AAC AGA AAA ATC C $^{3'}$
which hybridises to the eae gene;

$^{5'}$ TCG CTG AAT CCC CCT CCA TTA TGA CAG GCA $^{3'}$
which hybridises to the shiga-like toxin SltI gene; and

$^{5'}$ CAG GTA CTG GAT TTG ATT GTG ACA GTC ATT $^{3'}$
which hybridises to the shiga-like toxin SltII gene; and

the use of a method as any above for diagnosing an E.coli infection of a living animal body, including a human, or for the detection of E.coli contamination of consumables, such as meat, milk and vegetables.

The Invention

Conventional methods used to detect PCR amplification are laboursome, employ potentially carcinogenic substances (ethidium bromide gel electrophoresis), and are not suited as a routine assay method in the microbiological routine laboratory (68-72). This poses a serious problem, especially when potential pathogenic bacteria cannot be differentiated from facultative pathogenic or apathogenic ones due to characteristic biochemical, serological and/or morphological criteria. Thus, specific nucleic acid-based diagnostic methods that directly detect virulence factors or toxins harbored by these species are mandatory. This is in principal the case for the diagnosis of pathogenic *E.coli* bacteria. Biochemical properties of EHEC, EPEC, EIEC, ETEC, and EaggEC are not unique and cannot be used for setting them apart from other *E.coli* strains (54,60-62). Furthermore, virulence plasmids of *E.coli* can be found in other enterobacteria as well (38,48,83,88,89). Because of the diverse serological makeup, identification of pathogenic *E.coli* by serotyping is also not an accurate means of identification (12,15,28-32). Classical colony hybridization assays with probes specific for characteristic virulence factor and/or toxin genes are

laborous and timeconsuming (66,67). Classical PCR methods require various post-PCR steps in order to verify whether specific amplification of a target gene has occured (68-72). The TaqMan™-PCR detection system (74,75,90) enables the rapid, specific, sensitive, and high-throughput diagnosis for differentiation of pathogenic *E.coli* strains from other strains of E.coli. The assay has the ability to quantify the intial target sequence. Since PCR-reaction tubes have not to be opened after PCR cycling, the potential danger of cross-PCR contamination is almost neglegible. The scanning time of 96 samples is approximately 8 min, and calculation of test results can be automated with a commercially available spred sheet program. Thus, overall post-PCR processing time is cut to a minimum.

The TaqMan™-system relies on standard PCR technique with the addition of a specific internal fluorogenic oligonucleotide probe. The combination of conventional PCR with the Taq polymerase-dependent degradation of an internally hybridized oligonucleotide probe confers also specificity to this detection method, since it is highly unlikely that unspecific PCR amplification will yield positive fluorescence signals. Some rules for chosing the fluorigenic probes have to be obeyed (74,75). Criticial are the lenght of the probe, the location of reporter and quencher dyes and the absence of a guanosine at the 5´-end (74). Also, the distance of the probe from one of the specific PCR primers is important (Fig. 1, 2). This is due to the fact that the probe has to stay annealed to the template strand in order to be cleaved by Taq polymerase. Since annealing depends, at least partially, on the T_m of the probe, probes should be designed to have a higher T_m as the primers. According to the present invention this was solved (except for sltII) by designing probes that were 3 to 6 bp longer than the specific primers. PCR amplification includes extension of the target sequence after annealing of the primers and the T_m of the extended primers increases. For the fluorogenic oligonucleotide probe, where the 3´- end is capped in order to avoid elongation, the T_m remains constant, making it more likely that the probe dissociates before degradation by Taq polymerase. Oligonucleotide probe degradation can be optimized by spatial proximity of the fluorogenic probe and the primer. By moving the probe for sltI from 121 bp to 9 bp close to the primer, a significant improvement in ΔRQ values could be obtained (Fig. 2). A second strategy of optimization of TaqMan-™-PCR is to perform PCR elongation at 65°C, where it is also less likely that the probe dissociates from the template strand before Taq polymerase reaches and hydrolizes it. Values for ΔRQ can thus again be increased about 1.2 to 1.5 fold. The increase of ΔRQ values might be due to the ratio of

annealed oligonucleotide probe reached by Taq polymerase or to an increased processivity of Taq polymerase.

The concentration of fluorogenic probes influences the accuracy of TaqMan™-results. When the probe concentrations were > 50 pmol / PCR reaction only a relatively small fraction was hydrolysed by Taq polymerase. The ratio of undegraded probe to degraded probe remains high and the fluorescence emmission of the unquenched reporter dye does not significantly increase in relation to the fluorescence intensity of the reporter dye still close to the quencher. Thus, at high probe concentrations, ΔRQ values are lower than with intermediate probe concentrations (10 - 20 pmol, Fig. 3). When the probe concentration is too low, ΔRQ values are increased, however, variability of PCR results is increased, since probably small errors in pipeting or minimal differences between PCR reactions become critical (data not shown). Optimal probe concentration that yielded smallest variabilties and highest RQ values were found at a probe concentration of 20 pmol.

Since TaqMan™-PCR uses an internal oligonucleotide probe for detection of template amplification, specific primers and probes can be amply designed. The design of primer and probe sequences is especially important, when nucleotide sequence variants of a given gene exist. This is the case for sltI and sltII. For sltI, all published sequences were aligned and primers and probes were designed to bind to conserved regions of all three variants. For sltII, only one region of the published genes was conserved, thus this region was chosen for the fluorogenic oligonucleotide probe. The primers for amplification of sltII were designed to contain all possible nucleotide sequences at the ambiguous positions of the published sltII variants (degenerate primer approach) (79-83). By employing degenerate primers, it is possible to detect all published variants in one single PCR reaction.

The isolation method for template DNA affects the performance of the PCR. Two methods, that are suited as rapid purification steps for routine applications, namely boiling prep or spin prep were compared. Boiling preps may still contain some bacterial components that can affect PCR reactions, however, it is extremely fast. The spin prep method involves isolation steps that serve to purify DNA from potentially negatively influencing materials. ΔRQ values and sensitivity of TaqMan™-PCR for virulence genes from enterobacteria was not found significantly increased as compared to boiling preps when template DNA was prepared by spin prep method.

The overall sensitivity of TaqMan-PCR for all primer/probe combinations was comparable to visual scoring of PCR products by detection with ethidium bromide

stained agarose gel electrophoresis. Under optimized conditions, as few as 10^3 cfu sltI+ EHEC could be detected among 10^7 non-pathogenic *E.coli* per PCR reaction.

The use of immunomagnetic detection methods for E. coli O157 (54,91) has been put forward as a means to improve sensitivity of EHEC diagnostics by enrichment of this serogroup since the first slt producing strains were found to be O157:H7 positive (1,2). However, it is obvious that EHEC that are O157 antigen negative will be missed by this method. It became clear during serotyping studies of recent EHEC isolates that the number of O157+ EHEC now is small as compared to non-O157 EHEC (12,15,28,29,31). In a recent study, conducted in Southern Germany only 2 of 13 isolates were O157 positive (92). Immunomagnetic detection methods for other O serotypes are currently not available. Also, other enterobacteria such as *Citrobacter sp.* (83) and *Enterobacter sp.* (89) that can harbor shiga like toxins would be missed in the case of biased enrichment procedures previous to analysis of virulence genes. Thus, TaqMan™-based PCR that is designed for detection of virulence genes in all enterobacteria appears to be superior.

The infectious agents of a large proportion of diarrheal diseases is not known. Routine screening for bacterial pathogens in the gastrointestinal tract encompasses *Salmonella sp.*, *Shigella sp*, *S. aureus*, *Campylobacter sp.*, *Vibrio sp.*, *Yersinia sp.*, and *C. difficile* (32). It is well recognized that pathogenic *E.coli* such as ETEC, EHEC, EIEC, and EaggEC are important pathogens of the lower gastrointestinal tract and therefore might significantly contribute to the number of diarrheal infections (32). However, no routine bacteriological diagnostic procedures for these bacteria are performed, and, moreover, in most cases these pathogenic *E. coli* are misdiagnosed under the category of non-pathogenic "commensal flora". In order to address this problem a set of specific primers and fluorogenic probes were developed and optimized for TaqMan-™-based detection of virulence factors harbored by these bacteria (Tables 2 and 3). Arranging patient samples, positive and no-template controls of all 8 tested virulence genes in a standard 96 well microtiter format, a turnaround time from preparation of sample DNA to fluorescence measurement of under 5 hours can be achieved (Fig. 5). Thus, the TaqMan™-based assay for pathogenic E.coli provides an ultrarapid means of diagnosis of these bacteria. While being accurate, sensitive and specific, this assay requires minimal post-PCR processing time compared to conventional methods. When TaqMan-™ PCR is performed in optical tubes also the danger of cross-contamination of PCR reactions with amplified products is reduced to a minimum. Detection of virulence

plasmids harbored by pathogenic enterobacteria might prove the potential of these bacteria to cause disease in the host. It is not clear whether enterobacteria that contain toxin genes or attachment factors do also always express them outside the host. This might be an explanation why ELISA tests for shiga like toxins might be negative in a number of HUS cases where sltI and/or sltII containing EHECs can be detected by nucleic acid based methods.

The TaqMan™-assay according to the invention for detection of pathogenic E.coli was then tested in a routine diagnostic setting for the examination of stool samples obtained from children with diarrhea within a defined geographic area (Southern Bavaria) during a 7 month period. Results obtained by TaqMan™-PCR were compared to the standard detection method for PCR products (electrophoresis of ethidium stained agarose gels). 100 stool samples were analysed (Table 4). 22% of samples were found to test positive for one or more virulence factors. There were 2 cases of EHEC, 5 ETEC, 8 EaggEC, 1 EIEC, and 16 EPEC. This means that $^1/_5$ of children with diarrhea probably suffered from diarrhea caused by pathogenic *E.coli*. These numbers are far higher than these for all other groups of routinely screened bacterial gastrointestinal tract pathogens. Only 2 cases of salmonella and no campylobacter were observed within this group.

Interestingly, the two children diagnosed with EHEC were severely sick, one suffered from hemorrhagic colitis, the other developed HUS and had to be treated in a critical care unit.

Collectively, these investigations show that a large proportion of diarrheal diseases in children and also in adults are associated with pathogenic *E.coli* that are falsely diagnosed as commensal flora in standard microbiological procedures. The TaqMan™-methodology according to the invention for the first time enables the direct, fast, specific, and sensitive detection of these important pathogens. Moreover, virulence genes detected with this approach are not confined to *E.coli*, they also can be freely transmitted to other enterobacteria. Detection of the virulence genes within these bacteria would also be covered by the herein described TaqMan™-PCR. The assay requires only minimal post-PCR detection time, can thus be performed under 18 hours, and abolishes PCR-cross contamination problems.

According to the present invention *E.coli* virulence factor / toxin genes were used as targets for PCR amplification. PCR primers and fluorogenic probes were designed on the basis of published sequences. Eight different primer and probe sets for

detection of pathogenic groups of *E.coli* and related enterobacteria were specifically chosen, see table 1.

Group	Strain number	Serotype	Virulence factor / toxin
EHEC	1193/89	O157:H-	sltI, *eae*
	3574/92	O157:H7	sltII, *eae*
	A9167C	O157:H7	sltI,sltIIc, *eae*
	5769/87	O157:H7	sltI, sltII, *eae*
	427/89	O157:H-	sltI,sltIIc, *eae*
	1249/87	O157:H7	sltII, sltIIc, *eae*
ETEC	147/1	O128:H-	ST
	164/82	O148:H28	LT
EPEC	111/87	O111	EAF, *eae*
	12810	O114:H2	EAF, *eae*
EIEC	76-5	O143	*inv*-plasmid
	12860	O124	*inv*-plasmid
EaggEC			pCVD432 plasmid
control	ATCC 11775		--

Table 1: E.coli strains - virulence factors/toxins

Primer sequences and their locations with GenBank accessions are detailed in Table 2. Detection of EHEC sltI is based on consensus primer and probe sequences after alignment of sltI homologous genes (Genbank accessions Z36899, Z36900, and Z36901) (77,78). Detection of sltII variants is based on published sequences of homologous genes (Genbank accessions M76738, Z37725, L11079, X67515, M59432, M29153, M36727, and M21534) (79-83). For amplification of sltII, degenerate primer sets proved optimal. Diagnosis of ETEC is based on amplification of either heat labile (LT) (84) or heat stable toxin (ST) (36), EaggEC on pCVD432 plasmid sequences (40,50), EIEC on *inv*-plasmid sequences (38,48), EPEC on *E.coli* attaching and effacing gene (EAF plasmid) (37,85) or *E.coli* gene for EHEC attaching and effacing protein (*eae*) (86). PCR control amplification for integrity of DNA preparations was performed using primers specific for the *E.coli* parC gene (topoisomerase IV, Genbank accession M58408) (87).

Group	Virulence factor / toxin	Primer	Sequence (5′→3′)	location of primer	Size of PCR product	Gen-bankRef.	Ref.
ETEC	LT	LT-1	gcg tta cta tcc tct cta tgt g	874-895	339	S60731	(84)
		LT-2	agt ttt cca tac tga ttg ccg c	1213-1192			
	ST	ST-1	tcc ctc agg atg cta aac cag	100-120	260	M34916	(36)
		ST-2a	tcg att tat tca aca aag caa c	360-339			
EaggEC	pCVD432 plasmid	EA-1	ctg gcg aaa gac tgt atc att g	66-87	629	X81423	(40,50)
		EA-2	taa tgt ata gaa atc cgc tgt t	695-674			
EIEC	inv-plasmid	EI-1	ttt ctg gat ggt atg gtg agg	17786-17806	303	D50601 emb	(38,48)
		EI-2	ctt gaa cat aag gaa ata aac	18089-18069			
EPEC	EAF plasmid	EP-1	cag ggt aaa aga aag atg ata ag	546-568	398	X76137	(37,85)
		EP-2	aat atg ggg acc atg tat tat c	944-923			
	eae	EPeh-1	ccc gga ccc ggc aca agc ata ag	91-113	872	Z11541	(86)
		EPeh-2	agt ctc gcc agt att cgc cac c	963-942			
EHEC	sltI	sltI-1	atg aaa aaa aca tta tta ata gc	1113-1135	287	Z36899	(77,78)
		sltI-2	tca cyg agc tat tct gag tca acg	1400-1376			
	sltII	sltII-1	atg aag aag atr wtt rtd gcr	1148-1178	265	L11079	(79-83)
		sltII-2	gyt tta tty g tca gtc atw att aaa ctk cac yts rgc aaa kcc	1413-1385			
control	parC	par-1	aac ctg ttc agc gcc gca ttg	141-161	260	M58408	(87)
		par-2	aca acc ggg att cgg tgt aac	401-381			

Table 2: Primers for detection of pathogenic *E.coli*. W is A/T, R is A/G, D is A/G/T, Y is C/T and K is G/T.

Oligonucleotide probes and their Genbank Ref. Are shown in table 3. Oligonucleotide probes were designed (if possible) with a GC-content of 40-60%, no G-nucleotide at the 5´-end, length of probes was 27 to 30 bp. Probes were covalently conjugated with a fluorescent reporter dye (e.g. 6-carboxy-fluorescein [FAM]; λ_{em} = 518nm) and a fluorescent quencher dye (6-carboxytetram-ethyl-rhodamine [TAMRA]; λ_{em} = 582nm) at the most 5´ and most 3´ base, respectively. All primers and probes were obtained from Perkin Elmer, Germany.

Group	virulence factor / toxin	**Probe for Taqman™** (FAM-5´ → 3´-TAMRA)	bp	**Gen-bank Ref.**	Ref.
ETEC	LT	agc tcc cca gtc tat tac aga act atg	903-929	S60731	(84)
	ST	aca tac gtt aca gac ata atc aga atc ag	334-306	M34916	(36)
EaggEC	pCVD432 plasmid	ctc ttt taa ctt atg ata tgt aat gtc tgg	668-639	X81423	(40,50)
EIEC	inv - plasmid	caa aaa cag aag aac cta tgt cta cct	18063-18037	D50601 emb	(38,48)
EPEC	EAF - plasmid	ctt gga gtg atc gaa cgg gat cca aat	575-601	X76137	(37,85)
	eae	taa acg ggt att atc acc aga aaa atc c	935-908	Z11541	(86)
EHEC	sltI	tcg ctg aat ccc cct cca tta tga cag gca	1367-1338	Z36899	(77,78)
	sltII	cag gta ctg gat ttg att gtg aca gtc att	1371-1342	L11079	(79-83)
control	parC	atg tct gaa ctg ggc ctg aat gcc agc gcc	169-199	M58408	(87)

Table 3: TaqMan™-probes used for detection of pathogenic *E.coli*

TaqMan™-PCR was optimized by isolation of DNA from *E.coli* control strains harboring genes for LT, ST, *inv*-plasmid, pCVD342, EAF, *eae*, sltI and sltII (see Table 1). $MgCl_2$ concentrations were adjusted for maximum PCR product yields (as verified by agarose gel electrophoresis) and RQ values ($RQ=FAM_{fluorescence\ intensity}/TAMRA_{fluorescence\ intensity}$) with the above mentioned pathogenic *E.coli* control strains. Optimum PCR reactions for all primer / fluorigenic probes used were obtained at a $MgCl_2$ concentration of 5.2 mmol, 35 PCR cycles, an annealing temperature of 55°C and an extension temperature of 65°C. Extension at 65°C was found to yield higher RQ values, probably due to a lower rate of template/fluorogenic probe dissociation before degradation by Taq-polymerase.

The *E.coli* sltI gene was used as a target sequence for establishment of PCR and analysing different locations of probes relative to the PCR primers. Primers were designed to anneal in conserved regions of the sltI genes (see above). Two probes, sltI-N0 located 132 bp upstream of one primer and sltI-N1, placed at a 21 bp distance from the primer were compared (Fig. 1). RQ values achieved with probe sltI-N1(RQ_m= 6.3800) were reproducably found higher than RQ values generated with probe sltI-NO (RQ_m= 0.9620) at equal template concentrations of the *E.coli* sltI control DNA. Generally, also probes specific for other target genes that were located close (4 to 20 bp) to one of the two PCR primers yielded consistently higher RQ values than probes that were placed at a greater distance from the primers.

The influence of DNA preparation on the performance of TaqMan™-PCR was tested, since it has been reported that crude bacterial lysates can contain inhibiting factors that might interfere with PCR performance. Therefore, bacteria were collected after overnight growth on McConkey plates. DNA was prepared by boiling of bacteria inoculated in 0.9% NaCl solution or by isolation of genomic DNA with a commercial spin prep procedure (see the examples, material and methods). The RQ values and sensititvity of TaqMan™-PCR did not differ when the two preparation methods were compared. The RQ values obtained for PCR amplifications from DNA derived from 10^5 sltI or sltII containing EHEC prepared by boiling or by spin prep comparable.

The TaqMan™-PCR method relies on the detection of free reporter dye (FAM) that is released from the probe after hydrolysis. Thus, probe concentration should also have an effect on the assay performance by affecting the fraction of the probe that is degraded during PCR cycling. Probe concentrations were titrated in the range of 100 pmol to 0.1 pmol and ΔRQ values were determined. Optimal probe concentrations varied in between 10 pmol and 20 pmol depending on the target gene that was amplified (Fig. 3)

For testing sensitivity of TaqMan-PCR, EHEC containing either sltI or sltII were diluted in a suspension containing E.coli strain ATCC11775 at 10^7 cfu at log step dilutions. PCR was performed under optimized conditions and results from ethidium-bromide stained agarose gels were compared to TaqMan™ results. Minimum detection limits of a sltI containing EHEC strain was 10^3 cfu within 10^7. For sltII the detection limit was found at $10^{3.5}$ cfu in 10^7 enterobacteria. Both methods, detection

of PCR products by agarose gel electrophoresis and measurement of fluorescence signals by the TaqMan method yielded comparable results (Fig. 4), i.e. that at ΔRQ values above $\Delta RQ_{threshold}$ PCR product bands were visible in agarose gels, whereas at ΔRQ values around $\Delta RQ_{threshold}$ also in agarose gels PCR products were below the detection limit (Fig. 5). After optimizing detection tests for all virulence factors/toxins, TaqMan™-PCR was set up for routine testing of biological specimen for the presence of pathogenic E.coli bacteria (Fig. 5). Results of TaqMan™-PCR were compared to agarose gel electrophoresis.

The following examples will illustrate the invention further. They are, however, not to be construed as limiting.

Examples

Prevalence of pathogenic E.coli in stool specimens from children with diarrhea was tested using the method according to the invention.

In order to verify TaqMan™-PCR performance and to test for the occurence of pathogenic *E.coli* screening of 100 stool specimens from children of age 0 to 10 years with the clinical symptoms of diarrhea was undertaken. The materials and methods used in the test are described in more detail on page 22.

Collection of specimen took place fom June to October 1996. All samples in this study were derived from the area of Southern Bavaria. Stool specimen were plated on McConkey agar, incubated overnight and enterobacteria were collected. DNA was isolated and used as template in PCR reactions containing specific primers and fluorigenic probes for sltI, sltII, LT, ST, EAF-plasmid, eae-gene, inv-plasmid, and pCVD432. For verification of the integrity of DNA from individual preparations a control PCR reaction was set up, containing primers and an internal fluorigenic probe for amplification of the parC gene of *E.coli.* As a positive assay control, one PCR reaction was performed within each assay, where DNA from a positive control strain for the respective virulence factor/toxin was present. Applying this method reliable, specific and sensitive detection of all target genes could be achieved. Systematic analysis of 100 stool specimen derived from children suffering from diarrhea yielded 22 samples where one, two or three of the virulence factors/toxins of pathogenic *E.coli* could be detected. In detail, 2 patients harbored EHEC (one with hemorrhagic

colitis and one developed HUS). 3 patients tested positive for ETEC, 16 for EPEC, 1 for EIEC, and 8 for EaggEC (see Table 4). The patient suffering from hemorrhagic colitis tested positive for sltI and *eae*, the patient developing HUS tested positive for sltI, sltII and *eae*. One patient simultaneously harbored ETEC (LT+,ST+), EPEC (eae+), and EaggEC (pCVD342+), one patient tested positive for EIEC (inv+) and EaggEC (pCVD342+), two stool specimen contained EPEC (eae+) and EaggEC (pCVD342).

Enterobacteria from the two patients with EHEC were hybridized with sltI and sltII gene probes for testing accuracy and specificity of TaqMan™-PCR. In the case of patient one, where TaqMan™-PCR was positive for sltI, only colonies hybridizing with sltI could be found. Colonies of patient two, where TaqMan™-PCR was positive for sltI and sltII, hybridized with probes for sltI and sltII. Positive colonies were picked and biochemically typed as *E.coli*.

Antibiotic susceptibilty testing revealed that EHEC strains were sensitive to broad spectrum penicillins, cephalosporins and gyrase inhibitors.

Group	virulence factor / toxin	TaqMan: number of positive isolates	Agar gel electrophoresis : number of positive isolates	pathogenic group
ETEC	LT	2	2	5
	ST	3	3	
EaggEC	60 kb plasmid	8	8	8
EIEC	inv plasmid	1	1	1
EPEC	EAF plasmid	1	1	16
	eae	15	15	
EHEC	sltI	2	2	2
	sltII	1	1	
control	parC	100	100	

Table 4: Frequency of pathogenic *E.coli* in stool samples of children with diarrhea (n=100)

Materials and Methods

a) Bacterial strains, media, culture and DNA preparation: A number of EHEC, ETEC, EPEC, EIEC, and EaggEC *E.coli* strains were used as controls for accurate PCR amplification and were kindly provided by H. Karch, Würzburg, Germany and H. Beutin, Berlin, Germany (see Table 1) As a strain not harboring these virulence genes *E.coli* ATCC 11775 was used. For TaqMan™-PCR optimization, positive control strains were grown on McConkey agar (Becton Dickinson, Germany) at 37°C. After overnight culture, bacteria were collected and resuspended in 0.9% NaCl solution. Turbidity was adjusted to McFarland 0.5. DNA was either prepared by boiling (95°C, 10 min) or isolated using QiaAmp tissue kit spin prep columns (Qiagen, Germany). 10 µl of DNA suspension was used for PCR. Detection of pathogenic *E.coli* strains from stool specimen of humans or cows was performed after spreading an appropriate amount of stool on McConkey plates. After overnight culture all bacterial colonies from the surface of the McConkey plates were collected and processed as detailed above.

b) PCR-cyling: PCR recations were set up in 70µl final volume in thin-walled 0.2ml "optical PCR-tubes" (Perkin Elmer, Germany). The reaction mix contained: 10µl of bacterial lysate, 5.25 µl 25 mmol $MgCl_2$, 7 µl 10x PCR buffer, 40 pmol primers, 20 pmol specific fluorogenic probe, 150 µM of each dATP, dTTP, dGTP, dCTP (Perkin Elmer), 1 U AmpliTaq-Polymerase (Perkin Elmer). A Perkin Elmer model 9600 thermal cycler was used for PCR cycling. Initial denaturation of bacterial DNA was performed by heating for 5 min to 94°C. All cycles included a denaturation step for 15 sec at 94°C, annealing for 1 min 30 sec at 55°C, and extension for 1 min 30 sec at 65°C. 35 cycles were performed.

c) Post-PCR processing: After completion of cycling, the fluorescence intensities of the reporter dye, FAM, and the quencher dye, TAMRA, were determined using a Perkin Elmer LS50B luminiscence spectrophotometer equipped with a plate reader and modified for fluorescence measurements of PCR reactions in optical tubes. ΔRQ values were calculated as described in (74). A $\Delta RQ_{threshold}$ value was calculated on the basis of a 99% confidence interval above the mean of the triplicate no template controls ($\Delta RQ_{threshold} = 6{,}95 \times std_{mean\ of\ no\ template\ controls}$). PCR reactions were scored positive if $\Delta RQ_{sample} > \Delta RQ_{threshold}$ was given. For verification of the sensitivity of TaqMan™-measurements, PCR products were subjected to

agarose gel electrophoresis. 15 µl of sample were loaded with 2 µl sample buffer. PCR products were separated in 2% agarose gels containing ethidium bromide at 100V for 35 min. DNA was visualized under UV light and a digital image file was obtained using the Eagle Eyell System (Stratagene).

d) Verification of PCR amplificates: PCR products obtained from templates of respective positive control strains were directly subcloned into the TA cloning vector (Invitrogen, Germany) for verification of specificity of PCR amplification. After transfection ($CaCl_2$-method) of DH5α bacteria with the ligation products, plasmid containing bacteria were selected on ampicillin (Sigma, Germany) containing LB plates. Plasmid DNA was purified with Qiagen DNA purification columns (Quiagen, Germany). Inserts were PCR-cycle sequenced employing dideoxy-nucleotides conjugated to 4 dyes (DNA Dye terminator cycle sequencing kit, Perkin Elmer, Germany). Sequences were obtained with an Applied Biosystems model 373A (Applied Biosystems, Germany). Insert sequences were aligned to published sequences as referenced in Table 1 using the McDNAsis programme (Appligene, Great Britain). Sequence comparisons verified that the PCR products were identical to the respective virulence factors or toxins.

e) Sensitivity of TaqMan™ technique: For determination of the sensitivity of the TaqMan method, serial log-step dilutions of positive control strains were performed in a solution containing 10^7 cfu of E.coli reference strain ATCC 11775 DNA was either prepared by the boiling method (see above) or purified using spin prep columns designed for isolation of genomic bacterial DNA (Qiagen, Germany). Purification was according to the protocol of the manufacturer. The detection limit for sltI containing strains was determined with 10^3 cfu among 10^7 *E.coli* and for sltII containing strains as $10^{3.5}$ among 10^7.

f) Colony hybridisation and isolation of EHEC bacteria: EHEC bacterial strains and stool samples from patients testing positive in sltI or sltII TaqMan™-PCR were subjected to colony hybridisation. Briefly, bacteria were plated on McConkey agar plates such that single colonies could be seen. Bacteria were blotted on nylon membranes (Genescreen Plus, NEN, Germany), cracked (1% SDS), denatured (0.5M NaOH, 1.5M NaCl), neutralized (1M TRIS, 1.5M NaCl), and washed (20xSSC). Membranes were baked at 80°C for 2 hours. DNA probes specific for sltI or sltII were labelled with fluorescein (Gene-Images random prime labelling module, Amersham,

Germany). Afterwards, filters were hybridized with labelled probes. Hybridization was verified by non-radioactive detection system employing anti-FITC peroxidase mAb and ECL detection module (Gene-Images CDP-Star detection module, Amersham, Germany). Bacterial colonies hybridizing with the probe and non-hybridizing colonies were picked, verified by TaqMan-PCR and tested for antibiotic susceptibility.

Antibiotic susceptibility testing. EHEC and non-EHEC *E.coli* were picked from McConkey plates after testing for sltI or sltII or both toxin genes in colony hybridazation.and MIC testing was performed according to NCCLS guidelines for enterobacteria.

List of Drawings:

Fig. 1. Schematic map of parts of the sltI gene. Positions for the different sltI fluorogenic probes are given. Primers and pobes are not drawn to scale. Numbers refer to 5´and 3´ends of primers and probes.

Fig. 2. Effect of sltI fluorogenic probe positions on ΔRQ values. PCR was carried out as described in material and methods. ΔRQ values given are means of three independent emperiments +- std. Probe concentration was 20 pmol.

Fig. 3. Titration of optimal amount of fluorogenic probe concentrations. PCR was performed in the presence of 0.2, 2, 20 and 200 pmol of fluorogenic probes and appropriate primers. Template DNA was derived from E. coli positive control strains (see Table 1). No template controls for each probe concentration contained DNA from E.coli ATCC 11775.

Fig. 4 Sensitivity of TaqMan™-PCR. SltI and sltII positive control strains were titrated in log-dilutions in broth containing E.coli ATCC 11775 strain at 10^7 cfu. Serial dilutions of bacterial suspensions were plated on McConkey agar and grown overnight. Plates were swabbed, DNA was prepared by boiling prep. PCR was performed and TaqMan™- results were compared to conventional agarose gel electrophoresis.

Fig. 5 Flow chart and pipetting scheme for TaqMan™-PCR technique for detection *E.coli* virulence genes. Note that this assay can be performed as a routine diagnostic test under 18 hours.

References:

1. Centers for Disease Control.1982. Isolation of E. coli O157:H7 from sporadic cases of hemorrhagic colitis - United States. *MMWR. Morb. Mortal. Wkly. Rep.* 31:580, 585.

2. Karmali, M. A., M. Petric, C. Lim, P. C. Fleming, and B. T. Steele. 1983. Escherichia coli cytotoxin, haemolytic-uraemic syndrome, and haemorrhagic colitis [letter]. *Lancet* 2:1299.

3. Karmali, M. A., M. Petric, C. Lim, and P. C. Fleming. 1985. The association between idiopatic hemolitic uremic syndrom and infection by verotoxin-producing Escherichia coli. *J. Infect. Dis.* 151:775.

4. Riley, L. W., R. S. Remis, S. D. Helgerson, H. B. McGee, J. G. Wells, B. R. Davis, R. J. Hebert, E. S. Olcott, L. M. Johnson, N. T. Hargrett, P. A. Blake, and M. L. Cohen. 1983. Hemorrhagic colitis associated with a rare Escherichia coli serotype. *N. Engl. J. Med.* 308:681.

5. Pai, C. H., R. Gordon, H. V. Sims, and L. E. Bryan. 1984. Sporadic cases of hemorrhagic colitis associated with Escherichia coli 0157:H7. Clinical, epidemiologic, and bacteriologic features. *Ann. Intern. Med.* 101:738.

6. Borczyk, A. A., M. A. Karmali, H. Lior, and L. M. Duncan. 1987. Bovine reservoir for verotoxin-producing Escherichia coli O157: H7 [letter]. *Lancet* 1:98.

7. Blanco, J. E., M. Blanco, and J. Blanco. 1995. [Enterotoxigenic, verotoxigenic, and necrotoxigenic Escherichia coli in food and clinical samples. Role of animals as reservoirs of strains pathogenic for humans]. *Microbiologia.* 11:97.

8. Ostroff, S. M., P. M. Griffin, R. V. Tauxe, L. D. Shipman, K. D. Greene, J. G. Wells, J. H. Lewis, P. A. Blake, and J. M. Kobayashi. 1990. A statewide outbreak of Escherichia coli 0157:H7 infections in Washington State. *Am. J. Epidemiol.* 132:239.

9. Centers for Disease Control. 1993. Update: multistate outbreak of Escherichia coli O157:H7 infections from hamburgers-western United States, 1992-1993. *MMWR* 42:258.

10. Nathan, R. 1996. Japans E.coli outbreak elicits fear, anger. *Nature Medicine* 2:956.

11. Griffin, P. M., S. M. Ostroff, R. V. Tauxe, K. D. Greene, J. G. Wells, J. H. Lewis, and P. A. Blake. 1988. Illnesses associated with Escherichia coli 0157:H7 infections. A broad clinical spectrum. *Ann. Intern. Med.* 109:705.

12. Karmali, M. A. 1989. Infection by verocytotoxin-producing Escherichia coli. *Clin. Microbiol. Rev.* 2:15.

13. Kovacs, M. J., J. Roddy, S. Gregoire, W. Cameron, L. Eidus, and J. Drouin. 1990. Thrombotic thrombocytopenic purpura following hemorrhagic colitis due to Escherichia coli 0157:H7. *Am. J. Med.* 88:177.

14. O'Brien, A. D. and R. K. Holmes. 1987. Shiga and Shiga-like toxins. *Microbiol. Rev.* 51:206.

15. Karch, H. and J. Bockemühl. 1989. [Infections by enterohemorrhagic Escherichia coli (EHEC): a clinical and microbiologic problem and a challenge for the public health service]. *Immun. Infekt.* 17:206.

16. Siegler, R. L. 1995. The hemolytic uremic syndrome. *Pediatr. Clin. North Am.* 42:1505.

17. Rowe, P. C., W. Walop, H. Lior, and A. M. Mackenzie. 1991. Haemolytic anaemia after childhood Escherichia coli O 157 .H7 infection: are females at increased risk? *Epidemiol. Infect.* 106:523.

18. 1996. Häufung von EHEC-Erkrankungen in Bayern. *Münchner Ärztliche Anzeigen* 23:14.

19. Doyle, M. P. 1991. Escherichia coli O157:H7 and its significance in foods. *Int. J. Food Microbiol.* 12:289.

20. Belongia, E. A., K. L. MacDonald, G. L. Parham, K. E. White, J. A. Korlath, M. N. Lobato, S. M. Strand, K. A. Casale, and M. T. Osterholm. 1991. An outbreak of Escherichia coli O157:H7 colitis associated with consumption of precooked meat patties. *J. Infect. Dis.* 164:338.

21. O'Brien, A. D., A. R. Melton, C. K. Schmitt, M. L. McKee, M. L. Batts, and D. E. Griffin. 1993. Profile of Escherichia coli O157:H7 pathogen responsible for hamburger-borne outbreak of hemorrhagic colitis and hemolytic uremic syndrome in Washington. *J. Clin. Microbiol.* 31:2799.

22. Beutin, L., D. Geier, H. Steinruck, S. Zimmermann, and F. Scheutz. 1993. Prevalence and some properties of verotoxin (Shiga-like toxin)-producing Escherichia coli in seven different species of healthy domestic animals. *J. Clin. Microbiol.* 31:2483.

23. Martin, M. L., L. D. Shipman, J. G. Wells, M. E. Potter, K. Hedberg, I. K. Wachsmuth, R. V. Tauxe, J. P. Davis, J. Arnoldi, and J. Tilleli. 1986. Isolation of Escherichia coli O157:H7 from dairy cattle associated with two cases of haemolytic uraemic syndrome [letter]. *Lancet* 2:1043.

24. Besser, R. E., S. M. Lett, J. T. Weber, M. P. Doyle, T. J. Barrett, J. G. Wells, and P. M. Griffin. 1993. An outbreak of diarrhea and hemolytic uremic syndrome from Escherichia coli O157:H7 in fresh-pressed apple cider [see comments]. *JAMA* 269:2217.

25. Read, S. C., C. L. Gyles, R. C. Clarke, H. Lior, and S. McEwen. 1990. Prevalence of verocytotoxigenic Escherichia coli in ground beef, pork, and chicken in southwestern Ontario. *Epidemiol. Infect.* 105:11.

26. Gannon, V. P., R. K. King, J. Y. Kim, and E. J. Thomas. 1992. Rapid and sensitive method for detection of Shiga-like toxin-producing Escherichia coli in ground beef using the polymerase chain reaction. *Appl. Environ. Microbiol.* 58:3809.

27. Bopp, C. A., K. D. Greene, F. P. Downes, E. G. Sowers, J. G. Wells, and I. K. Wachsmuth. 1987. Unusual verotoxin-producing Escherichia coli associated with hemorrhagic colitis. *J. Clin. Microbiol.* 25:1486.

28. Farmer, J. J. and B. R. Davis. 1985. H7 antiserum-sorbitol fermentation medium: a single tube screening medium for detecting Escherichia coli O157:H7 associated with hemorrhagic colitis. *J. Clin. Microbiol.* 22:620.

29. Scotland, S. M., B. Rowe, H. R. Smith, G. A. Willshaw, and R. J. Gross. 1988. Vero cytotoxin-producing strains of Escherichia coli from children with haemolytic uraemic syndrome and their detection by specific DNA probes. *J. Med. Microbiol.* 25:237.

30. Scotland, S. M., G. A. Willshaw, H. R. Smith, B. Said, N. Stokes, and B. Rowe. 1993. Virulence properties of Escherichia coli strains belonging to serogroups O26, O55, O111 and O128 isolated in the United Kingdom in 1991 from patients with diarrhoea. *Epidemiol. Infect* 111:429.

31. Russmann, H., E. Kothe, H. Schmidt, S. Franke, D. Harmsen, A. Caprioli, and H. Karch. 1995. Genotyping of Shiga-like toxin genes in non-O157 Escherichia coli strains associated with haemolytic uraemic syndrome. *J. Med. Microbiol.* 42:404.

32. Koneman, E. W., S. D. Allen, W. M. Janda, P. C. Schreckenberger, and C. W. j. Washington. 1992. The Enterobacteriaceae. In Diagnostic Microbiology. J.B. Lippincott Company, Philadelphia. 132-133.

33. Edelman, R. and N. F. Pierce. 1984. From the National Institute of Allergy and Infectious Diseases. Summary of the 19th United States-Japan Joint Cholera Conference. *J. Infect. Dis.* 149:1014.

34. Hart, C. A., R. M. Batt, and J. R. Saunders. 1993. Diarrhoea caused by Escherichia coli. *Ann. Trop. Paediatr.* 13:121.

35. Chapman, P. A. and C. M. Daly. 1993. Evaluation of non-radioactive trivalent DNA probe (LT, ST1a, ST1b) for detecting enterotoxigenic Escherichia coli. *J. Clin. Pathol.* 46:309.

36. Moseley, S. L., J. W. Hardy, M. I. Hug, P. Echeverria, and S. Falkow. 1983. Isolation and nucleotide sequence determination of a gene encoding a heat-stable enterotoxin of Escherichia coli. *Infect. Immun.* 39:1167.

37. Jerse, A. E., J. Yu, B. D. Tall, and J. B. Kaper. 1990. A genetic locus of enteropathogenic Escherichia coli necessary for the production of attaching and effacing lesions on tissue culture cells. *Proc. Natl. Acad. Sci. U. S. A.* 87:7839.

38. Taylor, D. N., P. Echeverria, O. Sethabutr, C. Pitarangsi, U. Leksomboon, N. R. Blacklow, B. Rowe, R. Gross, and J. Cross. 1988. Clinical and microbiologic features of Shigella and enteroinvasive Escherichia coli infections detected by DNA hybridization. *J. Clin. Microbiol.* 26:1362.

39. Prats, G. and T. Llovet. 1995. [Enteroinvasive Escherichia coli. Pathogenesis and epidemiology]. *Microbiologia.* 11:91.

40. Nataro, J. P., Y. Deng, D. R. Maneval, A. L. German, W. C. Martin, and M. M. Levine. 1992. Aggregative adherence fimbriae I of enteroaggregative Escherichia coli mediate adherence to HEp-2 cells and hemagglutination of human erythrocytes. *Infect. Immun.* 60:2297.

41. Cohen, M. B., J. A. Hawkins, L. S. Weckbach, J. L. Staneck, M. M. Levine, and J. E. Heck. 1993. Colonization by enteroaggregative Escherichia coli in travelers with and without diarrhea. *J. Clin. Microbiol.* 31:351.

42. Chang, P. P., J. Moss, E. M. Twiddy, and R. K. Holmes. 1987. Type II heat-labile enterotoxin of Escherichia coli activates adenylate cyclase in human fibroblasts by ADP ribosylation. *Infect. Immun.* 55:1854.

43. Pickett, C. L., D. L. Weinstein, and R. K. Holmes. 1987. Genetics of type IIa heat-labile enterotoxin of Escherichia coli: operon fusions, nucleotide sequence, and hybridization studies. *J. Bacteriol.* 169:5180.

44. Giron, J. A., M. S. Donnenberg, W. C. Martin, K. G. Jarvis, and J. B. Kaper. 1993. Distribution of the bundle-forming pilus structural gene (bfpA) among enteropathogenic Escherichia coli. *J. Infect. Dis.* 168:1037.

45. Karch, H., J. Heesemann, R. Laufs, A. D. O'Brien, C. O. Tacket, and M. M. Levine. 1987. A plasmid of enterohemorrhagic Escherichia coli O157:H7 is required for expression of a new fimbrial antigen and for adhesion to epithelial cells. *Infect. Immun.* 55:455.

46. Nataro, J. P., M. M. Baldini, and J. B. Kaper. 1985. Detection of an Adherence Factor of Enteropathogenic Eschierichia coli with a DNA probe. *J. Infect. Dis.* 152:560.

47. Watanabe, H., E. Arakawa, K. Ito, J. Kato, and A. Nakamura. 1990. Genetic analysis of an invasion region by use of a Tn3-lac transposon and identification of a second positive regulator gene, invE, for cell invasion of Shigella sonnei: significant homology of invE with ParB of plasmid P1. *J. Bacteriol.* 172:619.

48. Sasakawa, C., K. Komatsu, T. Tobe, T. Suzuki, and M. Yoshikawa. 1993. Eight genes in region 5 that form an operon are essential for invasion of epithelial cells by Shigella flexneri 2a. *J. Bacteriol.* 175:2334.

49. Echeverria, P., O. Serichantalerg, S. Changchawalit, B. Baudry, M. M. Levine, F. Orskov, and I. Orskov. 1992. Tissue culture-adherent Escherichia coli in infantile diarrhea. *J. Infect. Dis.* 165:141.

50. Schmidt, H., C. Knop, S. Franke, S. Aleksic, J. Heesemann, and H. Karch. 1995. Development of PCR for screening of enteroaggregative Escherichia coli. *J. Clin. Microbiol.* 33:701.

51. Faruque, S. M., K. Haider, M. M. Rahman, A. R. Abdul Alim, A. H. Baqui, Q. S. Ahmad, K. M. Hossain, and M. J. Albert. 1992. Evaluation of a DNA probe to identify enteroaggregative Escherichia coli from children with diarrhoea in Bangladesh. *J. Diarrhoeal. Dis. Res.* 10:31.

52. Yamamoto, T., P. Echeverria, and T. Yokota. 1992. Drug resistance and adherence to human intestines of enteroaggregative Escherichia coli. *J. Infect. Dis.* 165:744.

53. Savarino, S. J., A. Fasano, J. Watson, B. M. Martin, M. M. Levine, S. Guandalini, and P. Guerry. 1993. Enteroaggregative Escherichia coli heat-stable enterotoxin 1 represents another subfamily of E. coli heat-stable toxin. *Proc. Natl. Acad. Sci. U. S. A.* 90:3093.

54. Bennett, A. R., S. MacPhee, and R. P. Betts. 1995. Evaluation of methods for the isolation and detection of Escherichia coli O157 in minced beef. *Lett. Appl. Microbiol.* 20:375.

55. March, S. B. and S. Ratnam. 1986. Sorbitol-MacConkey medium for detection of Escherichia coli O157: H7 associated with hemorrhagic colitis. *J. Clin. Microbiol.* 23:869.

56. Kleanthous, H., N. K. Fry, H. R. Smith, R. J. Gross, and B. Rowe. 1988. The use of sorbitol-MacConkey agar in conjunction with a specific antiserum for the detection of Vero cytotoxin-producing strains of Escherichia coli O 157. *Epidemiol. Infect.* 101:327.

57. March, S. B. and S. Ratnam. 1989. Latex agglutination test for detection of Escherichia coli serotype O157. *J. Clin. Microbiol.* 27:1675.

58. Beutin, L., S. Aleksic, S. Zimmermann, and K. Gleier. 1994. Virulence factors and phenotypical traits of verotoxigenic strains of Escherichia coli isolated from human patients in Germany. *Med. Microbiol. Immunol. Berl.* 183:13.

59. Stroeher, U. H., L. Bode, L. Beutin, and P. A. Manning. 1993. Characterization and sequence of a 33-kDa enterohemolysin (Ehly 1)-associated protein in Escherichia coli. *Gene* 132:89.

60. Johnson, R. P., R. J. Durham, S. T. Johnson, L. A. MacDonald, S. R. Jeffrey, and B. T. Butman. 1995. Detection of Escherichia coli O157:H7 in meat by an enzyme-linked immunosorbent assay, EHEC-Tek. *Appl. Environ. Microbiol.* 61:386.

61. Padhye, N. V. and M. P. Doyle. 1991. Rapid procedure for detecting enterohemorrhagic Escherichia coli O157:H7 in food. *Appl. Environ. Microbiol.* 57:2693.

62. Clark, C. G., S. Johnson, and R. P. Johnson. 1995. Further characterisation of a monoclonal antibody reactive with Escherichia coli O157:H7. *J. Med. Microbiol.* 43:262.

63. Karmali, M. A., M. Petric, M. Winkler, M. Bielaszewska, J. Brunton, N. van de Kar, T. Morooka, G. B. Nair, S. E. Richardson, and G. S. Arbus. 1994. Enzyme-linked immunosorbent assay for detection of immunoglobulin G antibodies to Escherichia coli Vero cytotoxin 1. *J. Clin. Microbiol.* 32:1457.

64. Gunzer, F., H. Bohm, H. Russmann, M. Bitzan, S. Aleksic, and H. Karch. 1992. Molecular detection of sorbitol-fermenting Escherichia coli O157 in patients with hemolytic-uremic syndrome. *J. Clin. Microbiol.* 30:1807.

65. Bockemuhl, J., S. Aleksic, and H. Karch. 1992. Serological and biochemical properties of Shiga-like toxin (verocytotoxin)-producing strains of Escherichia coli, other than O-group 157, from patients in Germany. *Int. J. Med. Microbiol. Virol. Parasitol. Infect. Dis.* 276:189.

66. Smith, H. R., S. M. Scotland, G. A. Willshaw, C. Wray, I. M. McLaren, T. Cheasty, and B. Rowe. 1988. Vero cytotoxin production and presence of VT genes in Escherichia coli strains of animal origin. *J. Gen. Microbiol.* 134:829.

67. Karch, H. and T. Meyer. 1989. Evaluation of oligonucleotide probes for identification of shiga-like-toxin-producing Escherichia coli. *J. Clin. Microbiol.* 27:1180.

68. Jackson, M. P. 1991. Detection of Shiga Toxin-Producing Shighella dysenteriae Type 1 and Escherichia Coli by Using Polymerase Chain Reaction with Incorporation of Digixigenin-11-dUTP. *J. Clin. Microbiol.* 29:1910.

69. Johnson, W. M., D. R. Pollard, H. Lior, S. D. Tyler, and K. R. Rozee. 1990. Differentiation of genes coding for Escherichia coli verotoxin 2 and the verotoxin associated with porcine edema disease (VTe) by the polymerase chain reaction. *J. Clin. Microbiol.* 28:2351.

70. Johnson, W. M., S. D. Tyler, G. Wang, and H. Lior. 1991. Amplification by the polymerase chain reaction of a specific target sequence in the gene coding for Escherichia coli verotoxin (VTe variant). *FEMS Microbiol. Lett.* 68:227.

71. Karch, H. and T. Meyer. 1989. Single primer pair for amplifying segments of distinct shiga-like-toxin genes by polymerase chain reaction. *J. Clin. Microbiol.* 27:2751.

72. Pollard, D. and W. M. Johnson. 1990. Rapid and Specific Detection of Verotoxin Genes in Escherichia Coli by the Polimerase Chain Reaction. *J. Clin. Microbiol.* 28:540.

73. Holland, P. M., R. D. Abramson, R. Watson, and D. H. Gelfand. 1991. Detection of specific polymerase chain reaction product by utilizing the 5'----3' exonuclease activity of Thermus aquaticus DNA polymerase. *Proc. Natl. Acad. Sci. U. S. A.* 88:7276.

74. Bassler, H. A., S. J. Flood, K. J. Livak, J. Marmaro, R. Knorr, and C. A. Batt. 1995. Use of a fluorogenic probe in a PCR-based assay for the detection of Listeria monocytogenes. *Appl. Environ. Microbiol.* 61:3724.

75. Livak, K. J., S. J. Flood, J. Marmaro, W. Giusti, and K. Deetz. 1995. Oligonucleotides with fluorescent dyes at opposite ends provide a quenched probe system useful for detecting PCR product and nucleic acid hybridization. *PCR. Methods Appl.* 4:357.

76. Förster, V. 1948. Zwischenmolekulare Energiewanderung und Fluoreszenz. *Annals of Physics (Leipzig)* 2:55.

77. Paton, A. W., J. C. Paton, P. N. Goldwater, and P. A. Manning. 1993. Direct detection of Escherichia coli Shiga-like toxin genes in primary fecal cultures by polymerase chain reaction. *J. Clin. Microbiol.* 31:3063.

78. Paton, A. W., J. C. Paton, P. N. Goldwater, M. W. Heuzenroeder, and P. A. Manning. 1993. Sequence of a variant Shiga-like toxin type-I operon of Escherichia coli O111:H-. *Gene* 129:87.

79. Paton, A. W., J. C. Paton, and P. A. Manning. 1993. Polymerase chain reaction amplification, cloning and sequencing of variant Escherichia coli Shiga-like toxin type II operons. *Microb. Pathog.* 15:77.

80. Gyles, C. L., S. A. De Grandis, C. MacKenzie, and J. L. Brunton. 1988. Cloning and nucleotide sequence analysis of the genes determining verocytotoxin production in a porcine edema disease isolate of Escherichia coli. *Microb. Pathog.* 5:419.

81. Gannon, V. P., C. Teerling, S. A. Masri, and C. L. Gyles. 1990. Molecular cloning and nucleotide sequence of another variant of the Escherichia coli Shiga-like toxin II family. *J. Gen. Microbiol.* 136:1125.

82. Schmitt, C. K., M. L. McKee, and A. D. O'Brien. 1991. Two copies of Shiga-like toxin II-related genes common in enterohemorrhagic Escherichia coli strains are responsible for the antigenic heterogeneity of the O157:H- strain E32511. *Infect. Immun.* 59:1065.

83. Schmidt, H., M. Montag, J. Bockemuhl, J. Heesemann, and H. Karch. 1993. Shiga-like toxin II-related cytotoxins in Citrobacter freundii strains from humans and beef samples. *Infect. Immun.* 61:534.

84. Inoue, T., T. Tsuji, M. Koto, S. Imamura, and A. Miyama. 1993. Amino acid sequence of heat-labile enterotoxin from chicken enterotoxigenic Escherichia coli is identical to that of human strain H 10407. *FEMS Microbiol. Lett.* 108:157.

85. Franke, J., H. Schmidt, and H. Karch. 1994. Nucleotide Sequence Analysis of Enteropathogenic Escherichia coli (EPEC) Adherence Factor Probe and

Development of PCR for Rapid Detection of EPEC Harboring Virulence Plasmids. *J. Clin. Microbiol.* 32:2460.

86. Yu, J. and J. B. Kaper. 1992. Cloning and characterization of the eae gene of enterohaemorrhagic Escherichia coli O157:H7. *Mol. Microbiol.* 6:411.

87. Kato, J., Y. Nishimura, R. Imamura, H. Niki, S. Hiraga, and H. Suzuki. 1990. New topoisomerase essential for chromosome segregation in E. coli [published erratum appears in Cell 1991 Jun 28;65(7):1289]. *Cell* 63:393.

88. Zhao, S., S. E. Mitchell, J. Meng, M. P. Doyle, and S. Kresovich. 1995. Cloning and nucleotide sequence of a gene upstream of the eaeA gene of enterohemorrhagic Escherichia coli O157:H7. *FEMS Microbiol. Lett.* 133:35.

89. Paton, A. W. and J. C. Paton. 1996. Enterobacter cloacae producing a shiga-like toxin II-related cytotoxinn associated with a case of hemolytic-uremic syndrome. *J. Clin. Microbiol.* 34:463.

90. Witham, P. K., K. J. Livak, C. A. Batt, and C. T. Yamashiro. 1996. A PCR-based assay for detection of Escherichia coli shiga-like toxin genes in ground beef. *Appl. Environ. Microbiol* 62:1347.

91. Karch, H., C. Janetzki-Mittmann, S. Aleksic, and M. Datz. 1996. Isolation of Enterohemorrhagic Escherichia coli O157 strains from patients with hemolytic-uremic symdrome by using immunomagnetic separation, DNA-based methods, and direct culture. *J. Clin. Microbiol.* 34:516.

92. Huppertz, H. I., D. Busch, H. Schmidt, S. Aleksic, and H. Karch. 1996. Diarrhea in young children associated with Escherichia coli non-O157 organisms that produce shiga-like toxin. *J. Pediatrics* 128:341.

1. A method for the detection of pathogenic E. coli in a sample comprising PCR amplification of DNA isolated from said sample using a set of oligonucleotide primers specific for virulence factors/toxins of pathogenic E.coli selected from

primers that hybridise to the gene encoding labile heat toxin, or stabile heat toxin for the amplification of a DNA sequence characteristic for enterotoxigenic E.coli;

primers that hybridise to the pCVD432 plasmid for the amplification of a DNA sequence characteristic for enteroaggregative E.coli;

primers that hybridise to the inv-plasmid for the amplification of a DNA sequence contained in enteroinvasive E.coli;

primers that hybridise to the EAF plasmid, or the eae gene for the amplification of a DNA sequence characteristic for enteropathogenic E.coli; and/or

primers that hybridise to the genes encoding shiga-like toxin sltI or sltII for the amplification of a DNA sequence characteristic for enterohemorrhagic E.coli, followed by detection and identification of the amplified product using conventional methods.

2. A method according to claim 1 wherein

the set of primers that hybridise to the gene encoding labile heat toxin is

LT-1: $^{5'}$ GCG TTA CTA TCC TCT CTA TGT G $^{3'}$ and
LT-2: $^{5'}$ AGT TTT CCA TAC TGA TTG CCG C $^{3'}$;

the set of primers that hybridise to the gene encoding stabile heat toxin is

ST-1: $^{5'}$ TCC CTC AGG ATG CTA AAC CAG $^{3'}$ and
ST-2a: $^{5'}$ TCG ATT TAT TCA ACA AAG CAA C $^{3'}$;

the set of primers which hybridise to the pCVD432 plasmid is

EA-1: $^{5'}$ CTG GCG AAA GAC TGT ATC ATT G $^{3'}$ and
EA-2: $^{5'}$ TAA TGT ATA GAA ATC CGC TGT T $^{3'}$;

the set of primers which hybridise to the inv-plasmid is

EI-1: $^{5'}$ TTT CTG GAT GGT ATG GTG AGG $^{3'}$ and
EI-2: $^{5'}$ CTT GAA CAT AAG GAA ATA AAC $^{3'}$;

the set of primers which hybridise to the EAF plasmid is

EP-1: $^{5'}$ CAG GGT AAA AGA AAG ATG ATA AG $^{3'}$ and
EP-2: $^{5'}$ AAT ATG GGG ACC ATG TAT TAT C $^{3'}$;

the set of primers which hybridise to the eae gene is

EPeh-1: $^{5'}$ CCC GGA CCC GGC ACA AGC ATA AG $^{3'}$ and
EPeh-2: $^{5'}$ AGT CTC GCC AGT ATT CGC CAC C $^{3'}$;

the primers which hybridises to the gene encoding shiga-like toxin SltI is

SltI-1: $^{5'}$ ATG AAA AAA ACA TTA TTA ATA GC $^{3'}$ and
SltI-2: $^{5'}$ TCA CYG AGC TAT TCT GAG TCA AGC $^{3'}$; and

the primers which hybridises to the gene encoding shiga-like toxin SltII is

SltII-1: $^{5'}$ ATG AAG AAG ATR WTT RTD GCR GYT TTA TTY G $^{3'}$ and
SltII-2: $^{5'}$ TCA GTC ATW ATT AAA CTK CAC YTS RGC AAA KCC $^{3'}$

wherein W is A/T, R is A/G, D is A/G/T, Y is C/T and K is G/T.

3. A method according to claims 1 to 2 wherein a polymerase having additional 5'-3' exonuclease activity is used for the amplification of DNA, and an oligonucleotide probe labelled at the most 5' base with a fluorescent dye and at the most 3' base with a fluorescent quencher dye which hybridises within the target DNA is included in the amplification process; said labelled oligonucleotide probe being susceptible to 5'-

3' exonuclease degradation by said polymerase to produce fragments that can be detected by fluorogenic detection methods.

4) A method according to claim 3 wherein the labelled oligonucleotide probe for the detection of labile heat toxin is

$^{5'}$ AGC TCC CCA GTC TAT TAC AGA ACT ATG $^{3'}$;

the labelled oligonucleotide probe for the detection of stabile heat toxin is

$^{5'}$ ACA TAC GTT ACA GAC ATA ATC AGA ATC AG $^{3'}$;

the labelled oligonucleotide probe for the detection of pCVD432 plasmid is

$^{5'}$ CTC TTT TAA CTT ATG ATA TGT AAT GTC TGG $^{3'}$;

the labelled oligonucleotide probe for the detection of the inv-plasmid is;

$^{5'}$ CAA AAA CAG AAG AAC CTA TGT CTA CCT $^{3'}$

the labelled oligonucleotide probe for the detection of the EAF-plasmid is;

$^{5'}$ CTT GGA GTG ATC GAA CGG GAT CCA AAT $^{3'}$;

the labelled oligonucleotide probe for the detection of the eae gene is

$^{5'}$ TAA ACG GGT ATT ATC AAC AGA AAA ATC C $^{3'}$;

the labelled oligonucleotide probe for the detection of shiga-like toxin SItI gene is

$^{5'}$ TCG CTG AAT CCC CCT CCA TTA TGA CAG GCA $^{3'}$; and

the labelled oligonucleotide probe for the detection of shiga-like toxin SItII gene is

$^{5'}$ CAG GTA CTG GAT TTG ATT GTG ACA GTC ATT $^{3'}$.

5) A method according to claims 3 to 4 wherein the fluoroscent reporter dye is 6-carboxy-fluoroscein, tetrachloro-6-carboxy-fluoroscein, or hexachloro-6-carboxy-fluoroscein, and the fluorescent quencher dye is 6-carboxytetramethyl-rhodamine.

6) A method according to claims 1 to 5 wherein the PCR amplification process consists of 35 PCR cycles at a $MgCl_2$ concentration of 5.2 mmol, an annealing temperature of 55 °C and an extension temperature of 65 °C.

7) A set of primers useful for PCR amplification of DNA specific for virulence factors/toxins of pathogenic E.coli selected from:

a set of primers that hybridise to the gene encoding labile heat toxin, or stabile heat toxin of enterotoxigenic E.coli;

a set of primers that hybridise to the pCVD432 plasmid of enteroaggregative E.coli;

a set of primers that hybridise to the inv-plasmid of enteroinvasive E.coli;

a set of primers that hybridise to the EAF plasmid, or the eae gene of enteropathogenic E.coli; and

a set of primers that hybridise to the gene encoding shiga-like toxin sltI or sltII of enterohemorrhagic E.coli,

8) A set of primers according to claim 7 wherein

the set of primers which hybridise to the gene encoding labile heat toxin is

LT-1: $^{5'}$ GCG TTA CTA TCC TCT CTA TGT G ^{3} and
LT-2: $^{5'}$ AGT TTT CCA TAC TGA TTG CCG C $^{3'}$;

the set of primers which hybridise to the gene encoding stabile heat toxin is

ST-1: $^{5'}$ TCC CTC AGG ATG CTA AAC CAG $^{3'}$ and
ST-2a: $^{5'}$ TCG ATT TAT TCA ACA AAG CAA C $^{3'}$;

the set of primers which hybridise to the pCVD432 plasmid is

EA-1: $^{5'}$ CTG GCG AAA GAC TGT ATC ATT G $^{3'}$ and
EA-2: $^{5'}$ TAA TGT ATA GAA ATC CGC TGT T $^{3'}$;

the set of primers which hybridise to the inv-plasmid is

EI-1: $^{5'}$ TTT CTG GAT GGT ATG GTG AGG $^{3'}$ and
EI-2: $^{5'}$ CTT GAA CAT AAG GAA ATA AAC $^{3'}$;

the set of primers which hybridise to the EAF plasmid is

EP-1: $^{5'}$ CAG GGT AAA AGA AAG ATG ATA AG $^{3'}$ and
EP-2: $^{5'}$ AAT ATG GGG ACC ATG TAT TAT C $^{3'}$;

the set of primers which hybridise to the eae gene is

EPeh-1: $^{5'}$ CCC GGA CCC GGC ACA AGC ATA AG $^{3'}$ and
EPeh-2: $^{5'}$ AGT CTC GCC AGT ATT CGC CAC C $^{3'}$;

the set of primers which hybridise to the shiga-like toxin sltI gene is

SltI-1: $^{5'}$ ATG AAA AAA ACA TTA TTA ATA GC $^{3'}$ and
SltI-2: $^{5'}$ TCA CYG AGC TAT TCT GAG TCA AGC $^{3'}$;

and

the set of primers which hybridise to the shiga-like toxin sltII is

SltII-1: $^{5'}$ ATG AAG AAG ATR WTT RTD GCR GYT TTA TTY G $^{3'}$ and
SltII-2: $^{5'}$ TCA GTC ATW ATT AAA CTK CAC YTS RGC AAA KCC $^{3'}$

wherein W is A/T, R is A/G, D is A/G/T, Y is C/T and K is G/T.

9) A set of primers according to claim 8 which in addition to the primers for amplification of target DNA comprise a labelled oligonucleotide probe which is labelled with a fluoroscent reporter dye, such as 6-carboxy-fluoroscein, tetrachloro-6-carboxy-fluoroscein, hexachloro-6-carboxy-fluoroscein, at the most 5' base and a fluoroscent quencher dye, such as 6-carboxytetramethyl-rhodamine, at the most 3' base, and have a nucleotide sequence selected from

5' AGC TCC CCA GTC TAT TAC AGA ACT ATG 3'
which hybridises to the gene encoding labile heat toxin;

5' ACA TAC GTT ACA GAC ATA ATC AGA ATC AG 3'
which hybridises to the gene encoding stabile heat toxin;

5' CTC TTT TAA CTT ATG ATA TGT AAT GTC TGG 3'
which hybridises to the pCVD432 plasmid;

5' CAA AAA CAG AAG AAC CTA TGT CTA CCT 3'
which hybridises to the inv-plasmid;

5' CTT GGA GTG ATC GAA CGG GAT CCA AAT 3'
which hybridises to the EAF plasmid;

5' TAA ACG GGT ATT ATC AAC AGA AAA ATC C 3'
which hybridises to the eae gene;

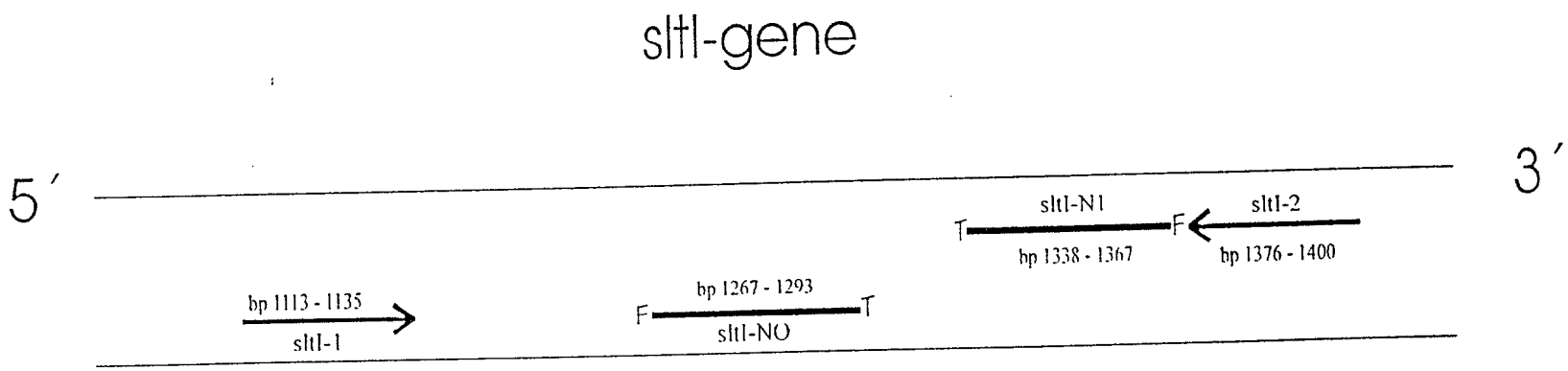
5' TCG CTG AAT CCC CCT CCA TTA TGA CAG GCA 3'
which hybridises to the shiga-like toxin SItI gene; and

5' CAG GTA CTG GAT TTG ATT GTG ACA GTC ATT 3'
which hybridises to the shiga-like toxin SItII gene.

10. The use of a method according to claims 1 to 6 for diagnosing an E.coli infection of a living animal body, including a human, or for the detection of E.coli contamination of consumables, such as meat, milk and vegetables.

Abstract

The present invention relates to a method for the detection of pathogenic E. coli in a sample comprising PCR amplification of DNA isolated from said sample using oligonucleotide primers specific for pathogenic E.coli.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3´
sltI-N1
T
F
sltI-2
bp 1338 - 1367
bp 1376 - 1400
bp 1113 - 1135
sltI-1
bp 1267 - 1293
F
T
sltI-NO

Figure 1

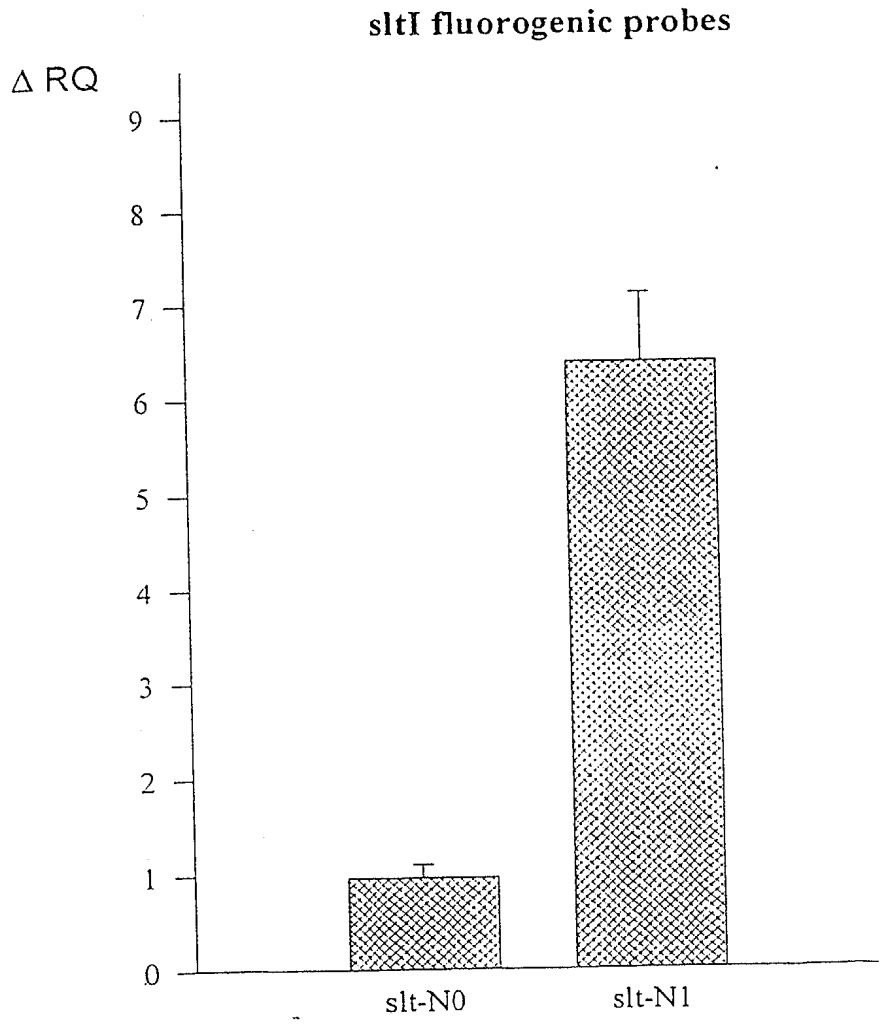
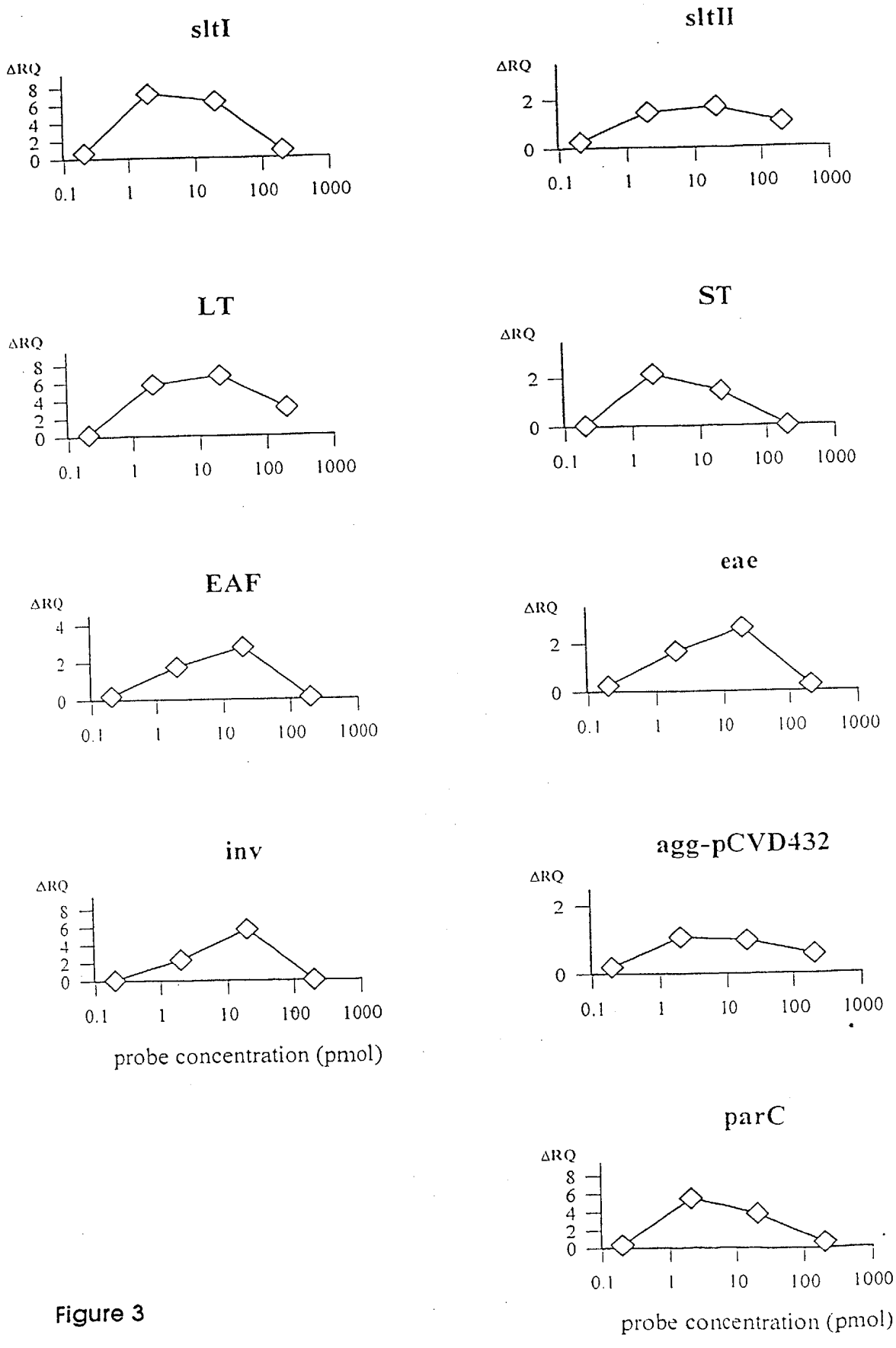


Figure 2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ΔRQ
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1
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ΔRQ
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10
100
1000
LT
ΔRQ
8
6
4
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0
0.1
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100
1000
ST
ΔRQ
2
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0.1
1
10
100
1000
EAF
ΔRQ
4
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eae
ΔRQ
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inv
ΔRQ
8
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4
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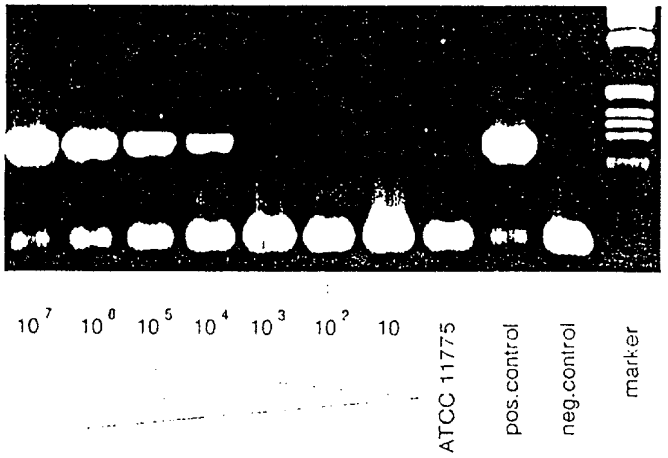
0
0.1
1
10
100
1000
probe concentration (pmol)
agg-pCVD432
ΔRQ
2
0
0.1
1
10
100
1000
parC
ΔRQ
8
6
4
2
0
0.1
1
10
100
1000
probe concentration (pmol)

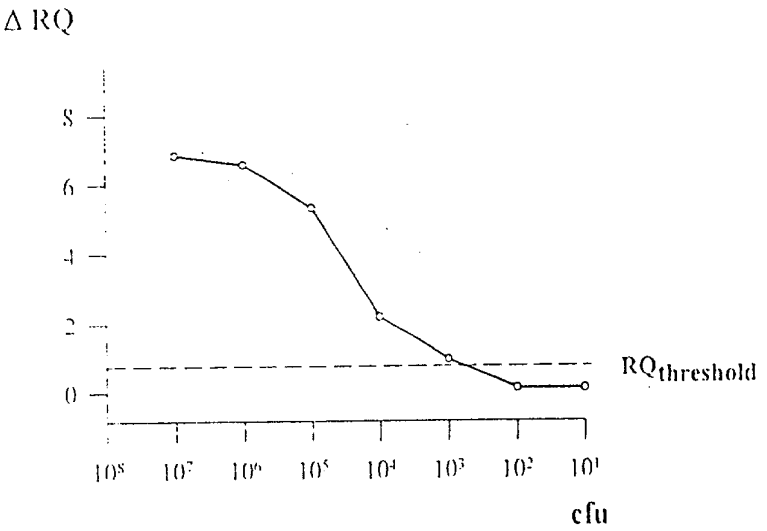
Figure 3

Figure 4

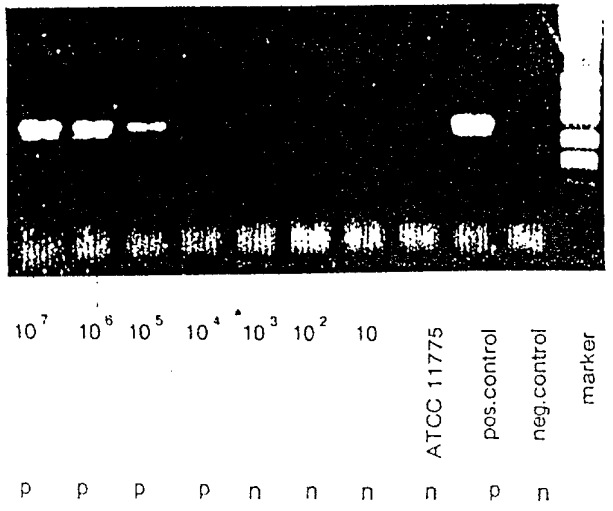
Sensitivity of TaqMan™-PCR

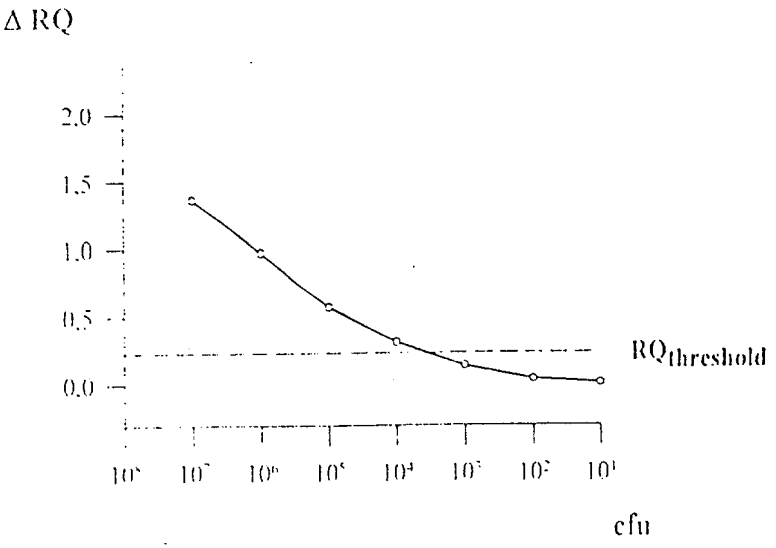
shiga like toxin I (slt I)

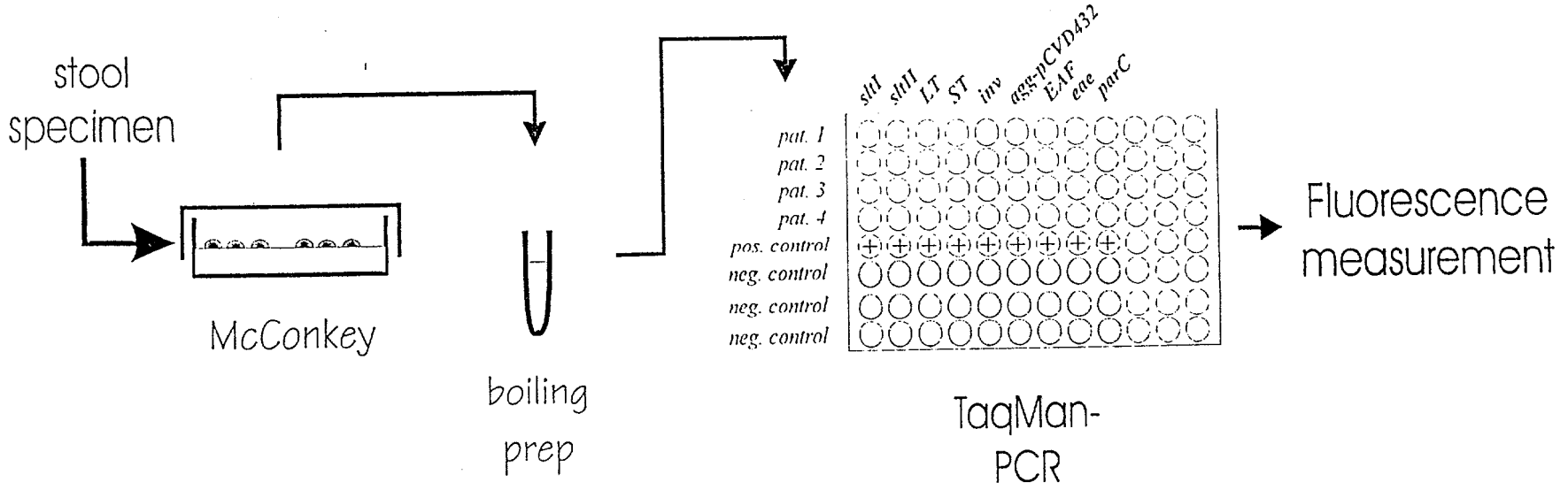




shiga like toxin II (slt II)



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specimen
McConkey
boiling
prep
stI
stII
LT
ST
inv
agg-pCVD432
EAF
eae
parC
pat. 1
pat. 2
pat. 3
pat. 4
pos. control
neg. control
neg. control
neg. control
TaqMan-
PCR
Fluorescence
measurement

Figure 5